

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 12:56:11 ; Search time 3039.87 Seconds  
(Without alignments)  
19183.272 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169  
Sequence: 1 atcttgttcagtttactctc.....cttgtgcctccatgctcag 6169

Scoring table: OLIGO-NUC  
Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 8

Total number of hits satisfying chosen parameters: 20439225

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

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256: em\_gss\_hum64:\*  
257: em\_gss\_hum65:\*  
258: em\_gss\_hum66:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	469	7.6	469	168	BF725009	bx1a12.y
2	429	7.0	429	168	BF725009	bx23h10.y
3	132	2.1	172	188	R95491	CBS-670 Sub
4	104	1.7	353	122	AW954907	EST366977
5	65	1.1	229	229	AQ526246	HS_5309_B
6	58	0.9	273	19	A1348766	ta85804.x
7	57	0.9	250	118	AW591614	x15902.x
8	56	0.9	415	188	R98218	y975a05.r1
9	56	0.9	465	228	AQ390434	CITR1-EL-
10	56	0.9	483	110	AM007449	W53107.x
11	56	0.9	486	224	AQ134263	HS_3047_B
12	56	0.9	519	122	AW962388	EST374461
13	55	0.9	525	110	AM024656	wu78h05.x
14	55	0.9	340	110	AV761433	AV761433
15	55	0.9	430	164	BE143811	MR0-HT016
16	55	0.9	447	1	AA055402	z174e10.s
17	55	0.9	578	105	AL038533	DKFP566E
18	55	0.9	879	232	AQ738799	HS_5386_B
19	54	0.9	459	228	AQ440412	HS_5070_B
20	53	0.9	350	5	AA318316	EST20383
21	53	0.9	360	234	AQ853189	DBS468P6
22	53	0.9	328	233	AQ784890	HS_3251_A
23	52	0.8	152	8	AA541310	n176b06.s
24	52	0.8	204	6	AA378330	EST91192
25	52	0.8	315	150	BF529627	602043852
26	52	0.8	375	13	AA916366	oe29b12.s
27	52	0.8	399	191	Z30246	HHEF028 Act
28	52	0.8	457	10	AA653459	ag66c11.s
29	52	0.8	552	9	AA594229	na29h05.s
30	52	0.8	570	229	AQ487554	RPCI-11-2
31	52	0.8	576	104	A1979101	wf70e01.x
32	51	0.8	376	114	AW301859	xr84d02.x
33	51	0.8	377	2	AA132947	zo19g08.s
34	51	0.8	437	2	AA131083	zo16b06.s
35	51	0.8	465	24	A1732596	zo19g08.x
36	50	0.8	389	230	AQ544057	RPCI-11-3
37	50	0.8	410	32	AV660235	AV660235
38	49	0.8	149	169	BF773353	CM3-TT004
39	49	0.8	208	224	AQ108180	CIT-HSP-2
40	49	0.8	312	122	AW897746	RCL-NN006
41	49	0.8	331	150	BF530611	602071889
42	49	0.8	331	20	A1445373	t124e08.x
43	49	0.8	331	188	T07225	EST05114 Fe
44	49	0.8	360	245	A2515814	RPCI-11-1
45	49	0.8	362	169	BF773297	CM3-TT004

## ALIGNMENTS

RESULT 1  
LOCUS BF725009 469 bp mRNA EST  
DEFINITION bx1a12.y1 Human iris cDNA (un-normalized, unamplified): BX Homo sapiens cDNA clone bx1a12 5', mRNA sequence.  
ACCESSION BF725009  
VERSION BF725009.1 GI:12040920  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 469)  
AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.  
TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics  
JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press  
COMMENT Contact: Wistow G

Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 11 row: a column: 12  
Seq primer: M13p1 reverse primer (ABI).  
Location/Qualifiers  
1. 469  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="bx1a12"  
/clone\_1lb="Human Iris cDNA (un-normalized, unamplified):  
BX"

## FEATURES

## SOURCE

BASE COUNT 107 a 149 c 136 g 77 t  
ORIGIN  
Query Match 7.6% Score 469; DB 168; Length 469;  
Best Local Similarity 100.0%; Pred. No. 6.3e-208;  
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
5273 caccatcagagcaccctcagacagagagcttcagaggaagctccacaaagctc 5332  
1 CACCATCAGGACGACCTTCAGACAGAGAGCTTCCAGAGGAAGCTCACAAGCTC 60  
5333 tgcgaatgaggtctctctgcaagctgctgagcttggcctgagatgacagctgtcca 5392  
61 TGCAATGAGGTTCTCTGTGACAGCTTGTGAGCTTGGCCTGAGATGCCAGCTGTCCA 120  
5393 gctgctgcttctgctgctcctcgtggtgagatgctggggcagagagctcagctaa 5452  
121 GCTGCTGCTTCTGCGCTCCTGCTGTGGATGTGGGGCCAGGAGAGCTCAGAGAA 180  
5453 ggcacatgaccagatgagcagatgacatgacatgacatgacatgacatgacatgac 5512  
181 GGCATATGACGAGTGGCCATGACATATACCTTACGTGTGGCAGTCCCAATGAATC 240  
5513 cagctgcccagagcagagcagagcagatgcaatgacatgacatgacatgacatgac 5572  
241 CAGCTGCCAGAGCAGACGACGACATGATCATTAACCTTAACAGAGAGACAGAG 300  
5573 caccacagccttagaactgagagcagacaaagctgacatgacatgacatgacatgac 5632  
301 CACCCAGCCTTAGACCTGAGGAGCCACCAAGCTGACCTGAGCTGAGAGAGCTCT 360  
5633 ccaccaatgacactgagcagagctgagcagagcccaagagagagagagagagagag 5692  
361 CCACCAATGACCTTGGACAGGCTGACAGGCCCCAGAGAGCCAGAGGAGCTGACAG 420  
5693 ggaactggcagccttggagcggagcggagcagcagctggaagaccccaaac 5741  
421 GGAGCTGGCAGCCCTGAGAGCGGAGCGGACGACAGCTGAGAAACCAAGC 469

RESULT	2	
LOCUS	BF726094	429 bp mRNA EST 05-JAN-2001
DEFINITION	bx23h10.y1 Human Iris cDNA (Un-normalized, unamplified): Bx Homo sapiens cDNA clone bx23h10 5', mRNA sequence.	
ACCESSION	BF726094	
VERSION	BF726094.1	GI:12042005
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 429)	
TITLE	Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.	
JOURNAL	NEIBANK: EST analysis and bioinformatics for ocular genomics invest. Ophthalmol. Vis. Sci. 41 (2000) in press	
COMMENT	Contact: Wistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 23 row: h column: 10 Seq primer: M13RPI reverse primer (ABI). Location/Qualifiers 1..429 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="bx23h10" /clone_11b="Human Iris cDNA (Un-normalized, unamplified): Bx" /tissue_type="Iris" /dev_stage="Adult" /lab_host="EMD110B" /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem Iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual ( <a href="http://www.lifetech.com/">http://www.lifetech.com/</a> ). First strand synthesis was carried out using a Not I primer-adaptor [5'-pCAGTAGTTCGATGCGACGGCGCCGCC(7)15-3'. Not I blunt end inserts were cloned into the Not I/EcoRV sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."	
FEATURES	source	
BASE COUNT	107 a 129 c 130 g 63 t	
ORIGIN		
Query Match	7.0%, Score 429; DB 166; Length 429;	
Best Local Similarity	100.0%; Prid. No. 3.2e-189;	
Matches 429; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
5303	cagcgtccagctgctgcttcctgcgcctccctcgtgtgtggatgtggggccagacagctc	5442
Db	1 CAGCTGTCACACTGCTGCTTTCTGGCCTCGCTGCTGTGGATGTGGGGCCAGACAGCTC	60
5443	agctcaggaagcccaatgacagagttgacgagtcagtcagtcacattcagttgycagctc	5502
Db	61 AGCTCAGGAAGGCCAATGACAGAGTGGCCGATGTCAGATATCCTTTCAGTGTGGCCAGTC	120
5503	ccaatgaaatccagctcgtgcccaagagcagagccaggtcagtcagtcacatcaactacaga	5562
Db	121 CCAATGAAATCCAGCTCGCCCAAGCAGACCCAGGCCATGTCAGTCACTCATTAACCTAACA	180
5563	gagacagcagcaccacagctcttagacctcggggggccacaaagctcagctacgtccctcgg	5622

D	b	181	GAGACGCGCACACCCTTGTAGACTTGAGGCGCACCAAAAGCTGCATCAGCTCCCTGG	240
O	y	5623	AAGAGCTCTCCACCAATGACTGTGACCGAGCTGCGGCCAAGGAGAACCCAGGAAG	5682
D	b	241	AAAAAAAACTTCACCAAAATTGACTTTGGACCAAGCTCTCCAGGCCCCAGAAACCCAGAGG	300
O	y	5683	ggctcgagaaggagactcgtggcaccccttaaggcgaaggaggggacacgcctggaaaccaaca	5742
D	b	301	GGCTGACAGAGGAGAGCTGGGGCACCCTTAGCGGGAGCGGGACCAAGCTTGGAAAACCAAACA	360
O	y	5743	gagaglttgagaactgcctcaacgaaccctctccagagacaagtcatlcttggaggaaagaga	5802
D	b	361	GAGAGTTGGAGACTGCTACAGAACCTCTCCGAGACAAGTCAGTTCTGGAGAGAAGA	420
O	y	5803	agaagcgac	5811
D	b	421	AGAAAGCGAC	429
R	E	S	RESULT	3
L	O	C	LOCUS	R95491
D	E	F	DEFINITION	R95491 172 bp mRNA EST 12-DEC-1995
A	C	S	ACCESSION	CBS-670 Subtractive cDNA library ocular ciliary body Homo sapiens
V	E	R	VERSION	R95491 CDS clone CBS-670 5', mRNA sequence.
K	E	Y	KEYWORDS	R95491.1 GI:975600 EST.
O	R	G	SOURCE	Homo sapiens human.
R	E	F	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
A	U	T	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
T	I	T	TITLE	1 (bases 1 to 172) Escribano,J., Ortego,J. and Coca-Prados,M. Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: Transcription and synthesis of plasma proteins J. Biochem. (Tokyo) 118 (5), 921-931 (1995)
J	O	U	JOURNAL	96318503
M	E	D	MEDLINE	Contact: Coca-Prados, M. Department of Ophthalmology and Visual Science Yale University Medical School 330 Cedar Street, New Haven, CT 06520-8061 Tel: 2037852742 Fax: 2037856123 Email: miguel_coca-prados@yale.edu
C	O	M	COMMENT	1-172 nt Seq primer: T3.
F	E	A	FEATURES	Location/Qualifiers
S	O	U	SOURCE	1..172 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CBS-670" /note="Vector: pluescript II SK. Site_1: EcoRI. Site_2: XhoI. A subtractive cDNA library was developed by hybridizing antisense, single-stranded phagemid DNA (ssDNA) (as pluescript SK-) from the ocular ciliary body cDNA library (target) of a 34-year-old female donor in lambda-uni-zap XR with biotinylated sense RNA of an ocular cell line cDNA library (driver) in the same vector."
B	A	S	BASE COUNT	54 a 37 c 61 g 20 t
O	R	I	ORIGIN	
Q	U	E	Query Match	2.1% Score 132 DB 188 Length 172:
B	E	S	Best local Similarity	100.0%; Pred. No. 2.8e-50;
M	A	T	Matches 132: Conservative	0; Mismatches 0; Indels 0; Gaps 0;
O	Y	5719	ggagcagcttgaaacccaacacagagatctggagactgtactacagacaacctcttcgag	5778
D	B	41	GGGACCAAGCTTGGAAACCAACAGAGAGCTTGGAGACTGCTACAGCAACTCTCCGAG	100
O	Y	5779	acaaagtcagttctgagagagaagaagcgaactaaggcaaanaatlgaatatctygcca	5838

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|||||
Db 101 ACAAGTCAGTTCTGAGCAAGAGCAAGCAGCTAAGCAAGAAATGAGAAATCTGGCCA 160
Oy 5839 ggaggttggaag 5850
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Db 161 GGAGGTTGAAA 172

RESULT 4
LOCUS AM954907 593 bp mRNA EST 01-JUN-2000
DEFINITION EST366977 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION AM954907
VERSION AM954907.1 GI:8144590
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 593)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
unpublished (2000)
TITLE
JOURNAL Contact: John Quackenbush
COMMENT The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 70
Seq primer: Reverse.
FEATURES
source 1. .593
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE resequences, MAGC"
/note="Vector: pBluescriptSkm"
BASE COUNT 151 a 142 c 180 g 120 t
ORIGIN
Query Match 1.7%: Score 104; DB 122; Length 593;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5837 caggaggttggaagcagagcagaggttagcagagctgtaggggagccgtgtcccca 5896
|||||
Db 42 CAGGAGGTTGAAAGACGACGACGAGAGTAGCAAGGCTGAGAGGGCGCGTGTCCCA 101
Oy 5897 gaccagagacactgctcgggctgtgtccacacagagctccagaagaag 5940
|||||
Db 102 CACCCGAGACACTCTCGCGCTGTGCCACGAGCTCCAGAGAAG 145

RESULT 5
LOCUS AO526246 420 bp DNA GSS 11-MAY-1999
DEFINITION HS.5309, B1.B04.SP66 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=885 COL=7 Row=D, DNA sequence.
ACCESSION AO526246
VERSION AO526246.1 GI:4773566
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 420)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

```

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|||||
TITLE Sequence-tagged connectors: A sequence approach to mapping and
JOURNAL scanning the human genome
MEDLINE Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT 99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (Info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 885 row: D column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 420.
FEATURES
source 1. .420
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="Plate=885 COL=7 Row=D"
/clone_id="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 117 a 92 c 109 g 102 t
ORIGIN
Query Match 1.1%: Score 65; DB 229; Length 420;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1459 ggcgcgtctgaactcctgactcaggtggtatccacccacccagcctcctaagtctgg 1518
|||||
Db 133 GCCTGGTTTAACCTCGACTCAGGTGATCCACCCACTCAGGCTCTTAAGTGTGG 74
Oy 1519 gattta 1523
|||||
Db 73 GATTA 69

RESULT 6
LOCUS A1348766 273 bp mRNA EST 18-MAR-1999
DEFINITION ta85a04.x2 NCI-CGAP_Brn20 Homo sapiens cDNA clone IMAGE:2050830 3',
similar to contains Alu repetitive element., mRNA sequence.
ACCESSION A1348766
VERSION A1348766.1 GI:4085984
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 273)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
Unpublished (1998)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps@mail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.
cDNA Library Preparation: David B. Kitzman, Ph.D.

```

CDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Insert length: 345 Std Error: 0.00  
Seq primer: -400p from Glibco

## FEATURES

## source

Location/Qualifiers  
1. 273  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2050830"  
/clone\_lib="NCI-CGAP\_Brn20"  
/tissue\_type="oligodendrogloma"  
/dev\_stage="adult"  
/lab\_host="DH108"  
/note="Organ: brain; Vector: PAMPI; mRNA made from  
oligodendrogloma tissue, cDNA made by oligo-dT priming.  
Directionally cloned. Size selected on agarose gel.  
Average insert size 500 bp. Primary library,  
non-amplified."  
BASE COUNT 119 a 46 c 63 g 45 t  
ORIGIN

Query Match 0.9%; Score 58; DB 19; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1326 agtctcgtgaacctcgtccaggtcaacaaattctcgtctcagctccgcg 1383  
|||||  
Db 86 AGCTCAGTCAACCTCTGCTCCAGGTCAACAAATCTCTGTCTCAGCTCCGCG 29

RESULT 7  
AM591614/c 250 bp mRNA EST 22-MAR-2000  
LOCUS AM591614.x1 NCI-CGAP-Ut1 Homo sapiens cDNA clone IMAGE:2837618 3'  
DERIVATION similar to contains Alu repetitive element; contains element MER40  
MER40 repetitive element; mRNA sequence.  
AM591614  
AM591614.1 GI:7278775  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 250)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA library Preparation: Life Technologies, Inc.  
CDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
image.llnl.gov/image/html/resources.shtml  
Seq primer: -400p from Glibco  
High quality sequence stop: 239.

## FEATURES

## source

Location/Qualifiers  
1. 250  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2837618"  
/clone\_lib="NCI-CGAP\_Ut1"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma; 7 pooled tumors"  
/lab\_host="DH108"

/note="Organ: uterus; Vector: PCMV-SPORE6; Site:1: SalI;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"  
BASE COUNT 88 a 48 c 45 g 69 t  
ORIGIN

Query Match 0.9%; Score 57; DB 118; Length 250;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1476 tgacctgaagtgatccaccaccctcagctcctcctaagtgctggatcacgacatga 1532  
|||||  
Db 250 TGACCTGAGGTGATCCACCACCTCAGCTCTCTAAAGTCTGGATTACAGCATGA 194

RESULT 8  
R98218 415 bp mRNA EST 11-SEP-1995  
LOCUS Y975a05.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone  
DEFINITION IMAGE:201584 5' similar to contains Alu repetitive element; mRNA  
sequence.  
R98218  
R98218.1 GI:983878  
EST.  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 415)  
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman  
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston  
, R., Williamson, A., Woldmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilison RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Insert Size: 833  
High quality sequence stops: 371  
Source: IMAGE Consortium, LLNL.  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 833 Std Error: 0.00  
Seq primer: M13Rp1  
High quality sequence stop: 371.

## FEATURES

## source

Location/Qualifiers  
1. 415  
/organism="Homo sapiens"  
/db\_xref="GDB:3770634"  
/db\_xref="taxon:9606"  
/clone="IMAGE:201584"  
/clone\_lib="Soares fetal liver spleen INFILS"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH108 (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
with a modified polylinker; Site:1: Pac I; Site:2: Eco RI;  
1st strand cDNA was primed with a Pac I - oligo(dT) primer  
(5' AACGCAAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'),  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 111 a 119 c 78 g 105 t 2 others  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 9,7e-15;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1326 agctactgcaacctgctccaggttcaagcaattctctgtctcagctccc 1381  
|||||  
Db 54 AGCTACTGCAACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTCAGCCTCCC 109

RESULT 9  
AO390434 465 bp DNA GSS 06-MAR-1999  
LOCUS CITBI-E1-2554E19.TR CITBI-E1 Homo sapiens genomic clone 2554E19,  
DEFINITION DNA sequence.  
ACCESSION AO390434.1 GI:4361457  
VERSION AO390434  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 465)  
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and  
Venter,J.C.  
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1997)  
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hneetlgr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.  
FEATURES  
source Location/Qualifiers  
1..465  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="2554E19"  
/clone\_1id="CITBI-E1"  
/sex="male"  
/cell\_type="sperm"  
/note="Vector: pBelobAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
Caltech Human BAC Library D"  
BASE COUNT 109 a 107 c 95 g 151 t 3 others  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 9,6e-15;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1326 agctactgcaacctgctccaggttcaagcaattctctgtctcagctccc 1381  
|||||  
Db 293 AGCTACTGCAACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTCAGCCTCCC 348

RESULT 10  
AM007449 483 bp mRNA EST 09-MAR-2000  
LOCUS w55h07.x1 NCI-CGAP-Panl Homo sapiens cDNA clone IMAGE:2511421 3'  
DEFINITION similar to contains Alu repetitive element; contains element MER18  
repetitive element ;, mRNA sequence.  
ACCESSION AM007449  
VERSION AM007449.1 GI:5856227  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 483)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Life Technologies catalog #: 11548-013  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution Information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bdrp/image/image.html  
Insert Length: 1365 Std Error: 0.00  
Seq primer: -40UP from Glbco  
High quality sequence stop: 412.  
FEATURES  
source Location/Qualifiers  
1..483  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2511421"  
/clone\_1id="NCI-CGAP-Panl"  
/issue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: pCMV-Sport6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"  
BASE COUNT 140 a 99 c 94 g 150 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 9,6e-15;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1327 gctcactgcaacctgctccaggttcaagcaattctctgtctcagctccc 1382  
|||||  
Db 365 GCTCAGTCACACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTCAGCCTCCG 420

RESULT 11  
AO134263 486 bp DNA GSS 23-SEP-1998  
LOCUS HS\_3047\_B1\_F02\_MF CIT Approved Human Genomic Sperm Library D Homo  
DEFINITION sapiens genomic clone Plate-3047 COL-3 Row-L, DNA sequence.  
ACCESSION AO134263  
VERSION AO134263.1 GI:3525629  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 486)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 3047 row: L column: 3  
Class: BAC ends

High quality sequence stop: 486.  
Location/Qualifiers  
1. 486  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 98 a 126 c 102 g 157 t 3 others

ORIGIN

Query Match 0.9% Score 56; DB 224; Length 486;  
Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1327 gctcactgcaacctctgcctccaggttcaagcaattctctctcagctcccg 1382  
|||||

Db 166 gctcactgcaacctctgcctccaggttcaagcaattctctcagctcccg 221  
|||||

RESULT 12  
AM962388 519 bp mRNA EST 01-JUN-2000  
LOCUS  
DEFINITION ESTJ14461 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM962388  
VERSION AM962388.1 GI:8152224  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 519)  
Hegde, P., Ol, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt  
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and  
Quackenbush, J.  
Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
Unpublished (2000)  
Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: john@tigr.org  
Plate: 174  
Seq primer: Reverse.  
Location/Qualifiers  
1. 519  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="MAGE resequences, MAGC"  
/note="Vector: pBluescriptskm"

BASE COUNT 147 a 125 c 132 g 115 t

ORIGIN

Query Match 0.9% Score 56; DB 122; Length 519;  
Best Local Similarity 100.0%; Pred. No. 9.5e-15;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1327 gctcactgcaacctctgcctccaggttcaagcaattctctcagctcccg 1382  
|||||

Db 324 gctcactgcaacctctgcctccaggttcaagcaattctctcagctcccg 269  
|||||

RESULT 13  
AM024656 525 bp mRNA EST 09-MAR-2000  
LOCUS  
DEFINITION AW7805.x1 NCI-CGAP\_K1d3 Homo sapiens cDNA clone IMAGE:2526201 3'  
Similar to contains Alu repetitive element; contains element LTR6

repetitive element ;, mRNA sequence.  
AM024656  
VERSION AM024656.1 GI:5878186  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 525)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bdnp/image/image.html](http://www-bio.llnl.gov/bdnp/image/image.html)  
Insert Length: 1276 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 458.  
Location/Qualifiers  
1. 525  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="IMAGE:2526201"  
/clone\_1lb="NCI-CGAP\_K1d3"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pTR73D-Pac (Pharmacia) with  
a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer,  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pTR73 vector. mRNA  
source: 2 pooled kidneys. Library went through one round  
of normalization. Library constructed by Bento Soares and  
M. Patricia Bonaldo."

BASE COUNT 149 a 113 c 104 g 159 t

ORIGIN

Query Match 0.9% Score 56; DB 110; Length 525;  
Best Local Similarity 100.0%; Pred. No. 9.5e-15;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1327 gctcactgcaacctctgcctccaggttcaagcaattctctcagctcccg 1382  
|||||

Db 362 gctcactgcaacctctgcctccaggttcaagcaattctctcagctcccg 417  
|||||

RESULT 14  
AV761433 340 bp mRNA EST 19-OCT-2000  
LOCUS  
DEFINITION AV761433 MDS Homo sapiens cDNA clone MDSBFA08 5', mRNA sequence.  
ACCESSION AV761433  
VERSION AV761433.1 GI:10919281  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 340)  
Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H.,  
Gu, Y., Li, N., Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng  
L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G.,  
Yang, Y., Gao, G., Zhang, Q., Chen, S., Han, Z. and Chen, Z.  
Homo sapiens cDNA MDS clones  
Unpublished (2000)



COMMENT Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
Source  
1. 340  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="MDSBEA08"  
/clone\_1lb="MDS"  
/tissue\_type="Bone marrow"  
/cell\_type="CD34+ hematopoietic stem/progenitor cell"  
/lab\_host="BM25.8"  
/note="Vector: pTRIPlex2; Site\_1: sf11A; Site\_2: sf11B"

BASE COUNT 96 a 87 c 96 g 61 t

ORIGIN

Query Match 0.9%; Score 55; DB 110; Length 340;  
Best Local Similarity 100.0%; Pred. No. 2.9e-14;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1327 gctcactgcaacctctgcctccaggttcaagcaattctctctgctcagctccc 1381  
|||||  
Db 228 gctcactgcaacctctgcctccaggttcaagcaattctctctgctcagctccc 174

RESULT 15  
BE143811  
LOCUS BE143811 430 bp mRNA EST 21-JUN-2000  
DEFINITION MRO-HT0164-021299-011-d07 HT0164 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE143811  
VERSION BE143811.1 GI:8606535  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 430)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Negal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
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Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=MRO-HT0164-021  
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Site\_2: SmaI: A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 85 a 121 c 103 g 121 t

ORIGIN

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Search completed: November 9, 2001, 00:19:58  
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